



#14

# SEQUENCE LISTING

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<120> MAMMALIAN CYTOKINES; RECEPTORS; RELATED REAGENTS AND METHODS

<130> dx01341

<140> 10/008566

<141> 2001-11-08

<150> US 60/298268

<151> 2001-06-14

<150> US 60/247218

<151> 2000-11-10

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<170> PatentIn version 3.1

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Asn Gly Asp Leu Glu Asp Ala Glu Leu Asp Asp Tyr Ser Phe Ser Cys  
30 35 40  
  
tat agc cag ttg gaa gtg aat gga tcg cag cat tca ctg acc tgt gct 196  
Tyr Ser Gln Leu Glu Val Asn Gly Ser Gln His Ser Leu Thr Cys Ala  
45 50 55  
  
ttt gag gac cca gat gtc aac acc acc aat ctg gaa ttt gaa ata tgt 244  
Phe Glu Asp Pro Asp Val Asn Thr Thr Asn Leu Glu Phe Glu Ile Cys  
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Gly Ala Leu Val Glu Val Lys Cys Leu Asn Phe Arg Lys Leu Gln Glu  
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Ile Tyr Phe Ile Glu Thr Lys Lys Phe Leu Leu Ile Gly Lys Ser Asn	
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Ile Cys Val Lys Val Gly Glu Lys Ser Leu Thr Cys Lys Lys Ile Asp	
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Leu Thr Thr Ile Val Lys Pro Glu Ala Pro Phe Asp Leu Ser Val Ile	
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Tyr Arg Glu Gly Ala Asn Asp Phe Val Val Thr Phe Asn Thr Ser His	
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Gln Glu Lys Asp Glu Asn Lys Trp Thr His Val Asn Leu Ser Ser Thr	
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Lys Leu Thr Leu Leu Gln Arg Lys Leu Gln Pro Ala Ala Met Tyr Glu	
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Ile Lys Val Arg Ser Ile Pro Asp His Tyr Phe Lys Gly Phe Trp Ser	
205 210 215	
gaa tgg agt cca agt tat tac ttc aga act cca gag atc aat aat agc	724
Glu Trp Ser Pro Ser Tyr Tyr Phe Arg Thr Pro Glu Ile Asn Asn Ser	
220 225 230	
tca ggg gag atg gat cct atc tta cta acc atc agc att ttg agt ttt	772
Ser Gly Glu Met Asp Pro Ile Leu Leu Thr Ile Ser Ile Leu Ser Phe	
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Phe Ser Val Ala Leu Leu Val Ile Leu Ala Cys Val Leu Trp Lys Lys	
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agg att aag cct atc gta tgg ccc agt ctc ccc gat cat aag aag act	868
Arg Ile Lys Pro Ile Val Trp Pro Ser Leu Pro Asp His Lys Lys Thr	
270 275 280	
ctg gaa cat ctt tgt aag aaa cca aga aaa aat tta aat gtg agt ttc	916
Leu Glu His Leu Cys Lys Lys Pro Arg Lys Asn Leu Asn Val Ser Phe	
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Lys	Cys	Leu	Asn	Phe	Arg	Lys	Leu	Gln	Glu	Ile	Tyr	Phe	Ile	Glu	Thr				
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Glu	Lys	Ser	Leu	Thr	Cys	Lys	Lys	Ile	Asp	Leu	Thr	Thr	Ile	Val	Lys				
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Pro	Glu	Ala	Pro	Phe	Asp	Leu	Ser	Val	Ile	Tyr	Arg	Glu	Gly	Ala	Asn				
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Asp	Phe	Val	Val	Thr	Phe	Asn	Thr	Ser	His	Leu	Gln	Lys	Lys	Tyr	Val				
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Lys	Val	Leu	Met	His	Asp	Val	Ala	Tyr	Arg	Gln	Glu	Lys	Asp	Glu	Asn				
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Lys	Trp	Thr	His	Val	Asn	Leu	Ser	Ser	Thr	Lys	Leu	Thr	Leu	Leu	Gln				
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Arg	Lys	Leu	Gln	Pro	Ala	Ala	Met	Tyr	Glu	Ile	Lys	Val	Arg	Ser	Ile				
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Val	Ile	Leu	Ala	Cys	Val	Leu	Trp	Lys	Lys	Arg	Ile	Lys	Pro	Ile	Val				
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Lys Pro Arg Lys Asn Leu Asn Val Ser Phe Asn Pro Glu Ser Phe Leu  
 290 295 300

Asp Cys Gln Ile His Arg Val Asp Asp Ile Gln Ala Arg Asp Glu Val  
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Glu Gly Phe Leu Gln Asp Thr Phe Pro Gln Gln Leu Glu Glu Ser Glu  
 325 330 335

Lys Gln Arg Leu Gly Gly Asp Val Gln Ser Pro Asn Cys Pro Ser Glu  
 340 345 350

Asp Val Val Val Thr Pro Glu Ser Phe Gly Arg Asp Ser Ser Leu Thr  
 355 360 365

Cys Leu Ala Gly Asn Val Ser Ala Cys Asp Ala Pro Ile Leu Ser Ser  
 370 375 380

Ser Arg Ser Leu Asp Cys Arg Glu Ser Gly Lys Asn Gly Pro His Val  
 385 390 395 400

Tyr Gln Asp Leu Leu Leu Ser Leu Gly Thr Thr Asn Ser Thr Leu Pro  
 405 410 415

Pro Pro Phe Ser Leu Gln Ser Gly Ile Leu Thr Leu Asn Pro Val Ala  
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Gln Gly Gln Pro Ile Leu Thr Ser Leu Gly Ser Asn Gln Glu Glu Ala  
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gaa ggt cac act tcg ggg tgc ctc cta gac gca gag cag cga gac gac Glu Gly His Thr Ser Gly Cys Leu Leu Asp Ala Glu Gln Arg Asp Asp 80 85 90	291
att ctc tat ttc tcc atc agg aat ggg acg cac ccc gtt ttc acc gca Ile Leu Tyr Phe Ser Ile Arg Asn Gly Thr His Pro Val Phe Thr Ala 95 100 105	339
agt cgc tgg atg gtt tat tac ctg aaa ccc agt tcc ccg aag cac gtg Ser Arg Trp Met Val Tyr Tyr Leu Lys Pro Ser Ser Pro Lys His Val 110 115 120 125	387
aga ttt tcg tgg cat cag gat gca gtg acg gtg acg tgt tct gac ctg Arg Phe Ser Trp His Gln Asp Ala Val Thr Val Thr Cys Ser Asp Leu 130 135 140	435
tcc tac ggg gat ctc ctc tat gag gtt cag tac cgg agc ccc ttc gac Ser Tyr Gly Asp Leu Leu Tyr Glu Val Gln Tyr Arg Ser Pro Phe Asp 145 150 155	483
acc gag tgg cag tcc aaa cag gaa aat acc tgc aac gtc acc ata gaa Thr Glu Trp Gln Ser Lys Gln Glu Asn Thr Cys Asn Val Thr Ile Glu 160 165 170	531
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ctg gcc atc ctt ctg atg gtg tct ctc ctc ctt ctg tct tta tgg aaa Leu Ala Ile Leu Leu Met Val Ser Leu Leu Leu Leu Ser Leu Trp Lys 240 245 250	771

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Leu Trp Arg Val Lys Lys Phe Leu Ile Pro Ser Val Pro Asp Pro Lys	
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Ser Ile Phe Pro Gly Leu Phe Glu Ile His Gln Gly Asn Phe Gln Glu	
270 275 280 285	

tgg atc aca gac acc cag aac gtg gcc cac ctc cac aag atg gca ggt	915
Trp Ile Thr Asp Thr Gln Asn Val Ala His Leu His Lys Met Ala Gly	
290 295 300	

gca gag caa gaa agt ggc ccc gag gag ccc ctg gta gtc cag ttg gcc	963
Ala Glu Gln Glu Ser Gly Pro Glu Glu Pro Leu Val Val Gln Leu Ala	
305 310 315	

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Lys Thr Glu Ala Glu Ser Pro Arg Met Leu Asp Pro Gln Thr Glu Glu	
320 325 330	

aaa gag gcc tct ggg gga tcc ctc cag ctt ccc cac cag ccc ctc caa	1059
Lys Glu Ala Ser Gly Gly Ser Leu Gln Leu Pro His Gln Pro Leu Gln	
335 340 345	

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350 355 360 365	

cgc tcc tac gtg gcg ttg tgaatggacac accactgtca aagtcaacgt	1155
Arg Ser Tyr Val Ala Leu	
370	

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Ser Lys Tyr Ser Arg Thr Asn Leu Thr Phe His Tyr Arg Phe Asn Gly  
50 55 60

Asp Glu Ala Tyr Asp Gln Cys Thr Asn Tyr Leu Leu Gln Glu Gly His  
65 70 75 80

Thr Ser Gly Cys Leu Leu Asp Ala Glu Gln Arg Asp Asp Ile Leu Tyr  
85 90 95

Phe Ser Ile Arg Asn Gly Thr His Pro Val Phe Thr Ala Ser Arg Trp  
100 105 110

Met Val Tyr Tyr Leu Lys Pro Ser Ser Pro Lys His Val Arg Phe Ser  
115 120 125

Trp His Gln Asp Ala Val Thr Val Thr Cys Ser Asp Leu Ser Tyr Gly  
130 135 140

Asp Leu Leu Tyr Glu Val Gln Tyr Arg Ser Pro Phe Asp Thr Glu Trp  
145 150 155 160

Gln Ser Lys Gln Glu Asn Thr Cys Asn Val Thr Ile Glu Gly Leu Asp  
165 170 175

Ala Glu Lys Cys Tyr Ser Phe Trp Val Arg Val Lys Ala Met Glu Asp  
180 185 190

Val Tyr Gly Pro Asp Thr Tyr Pro Ser Asp Trp Ser Glu Val Thr Cys  
195 200 205

Trp Gln Arg Gly Glu Ile Arg Asp Ala Cys Ala Glu Thr Pro Thr Pro  
210 215 220

Pro Lys Pro Lys Leu Ser Lys Phe Ile Leu Ile Ser Ser Leu Ala Ile  
225 230 235 240

Leu Leu Met Val Ser Leu Leu Leu Leu Ser Leu Trp Lys Leu Trp Arg  
245 250 255

Val Lys Lys Phe Leu Ile Pro Ser Val Pro Asp Pro Lys Ser Ile Phe  
260 265 270



Pro Gly Leu Phe Glu Ile His Gln Gly Asn Phe Gln Glu Trp Ile Thr  
 275 280 285

Asp Thr Gln Asn Val Ala His Leu His Lys Met Ala Gly Ala Glu Gln  
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Glu Ser Gly Pro Glu Glu Pro Leu Val Val Gln Leu Ala Lys Thr Glu  
 305 310 315 320

Ala Glu Ser Pro Arg Met Leu Asp Pro Gln Thr Glu Glu Lys Glu Ala  
 325 330 335

Ser Gly Gly Ser Leu Gln Leu Pro His Gln Pro Leu Gln Gly Gly Asp  
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 Ile Phe Ile Leu Gln Leu Val Gly Leu Val Leu Thr Tyr Asp Phe Thr  
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 Asn Cys Asp Phe Glu Lys Ile Lys Ala Ala Tyr Leu Ser Thr Ile Ser  
 35 40 45  
 aaa gac ctg att aca tat atg agt ggg acc aaa agt acc gag ttc aac 192  
 Lys Asp Leu Ile Thr Tyr Met Ser Gly Thr Lys Ser Thr Glu Phe Asn  
 50 55 60  
 aac acc gtc tct tgt agc aat cgg cca cat tgc ctt act gaa atc cag 240  
 Asn Thr Val Ser Cys Ser Asn Arg Pro His Cys Leu Thr Glu Ile Gln  
 65 70 75 80  
 agc cta acc ttc aat ccc acc gcc ggc tgc gcg tcg ctc gcc aaa gaa 288

Ser	Leu	Thr	Phe	Asn	Pro	Thr	Ala	Gly	Cys	Ala	Ser	Leu	Ala	Lys	Glu	
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Met	Phe	Ala	Met	Lys	Thr	Lys	Ala	Ala	Leu	Ala	Ile	Trp	Cys	Pro	Gly	
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Tyr	Ser	Glu	Thr	Gln	Ile	Asn	Ala	Thr	Gln	Ala	Met	Lys	Lys	Arg	Arg	
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aaa	agg	aaa	gtc	aca	acc	aat	aaa	tgt	ctg	gaa	caa	gtg	tca	caa	tta	432
Lys	Arg	Lys	Val	Thr	Thr	Asn	Lys	Cys	Leu	Glu	Gln	Val	Ser	Gln	Leu	
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caa	gga	ttg	tgg	cgt	cgc	ttc	aat	cga	cct	tta	ctg	aaa	caa	cag	taa	480
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Asn	Cys	Asp	Phe	Glu	Lys	Ile	Lys	Ala	Ala	Tyr	Leu	Ser	Thr	Ile	Ser	
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Lys	Asp	Leu	Ile	Thr	Tyr	Met	Ser	Gly	Thr	Lys	Ser	Thr	Glu	Phe	Asn	
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Ser	Leu	Thr	Phe	Asn	Pro	Thr	Ala	Gly	Cys	Ala	Ser	Leu	Ala	Lys	Glu	
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Met	Phe	Ala	Met	Lys	Thr	Lys	Ala	Ala	Leu	Ala	Ile	Trp	Cys	Pro	Gly	
			100					105					110			
Tyr	Ser	Glu	Thr	Gln	Ile	Asn	Ala	Thr	Gln	Ala	Met	Lys	Lys	Arg	Arg	
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Lys	Arg	Lys	Val	Thr	Thr	Asn	Lys	Cys	Leu	Glu	Gln	Val	Ser	Gln	Leu	
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145 150 155